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Abstract: Single nucleotide polymorphisms (SNPs) are appealing genetic markers due to several beneficial attributes, but uncertainty remains about how many of these bi-allelic markers are necessary to have sufficient power to differentiate populations, a task now generally accomplished with highly polymorphic microsatellite markers. In this study, we tested the utility of 37 SNPs and 13 microsatellites for differentiating 29 broadly distributed populations of Chinook salmon (n = 2783). Information content of all loci was determined by In and G'ST, and the top 12 markers ranked by In were microsatellites, but the 6 highest, and 7 of the top 10 G'ST ranked markers, were SNPs. The mean ratio of random SNPs to random microsatellites ranged from 3.9 to 4.1, but this ratio was consistently reduced when only the most informative loci were included. Individual assignment test accuracy was higher for microsatellites (73.1%) than SNPs (66.6%), and pooling all 50 markers provided the highest accuracy (83.2%). When marker types were combined, as few as 15 of the top ranked loci provided higher assignment accuracy than either microsatellites or SNPs alone. Neighbour-joining dendrograms revealed similar clustering patterns and pairwise tests of population differentiation had nearly identical results with each suite of markers. Statistical tests and simulations indicated that closely related populations were better differentiated by microsatellites than SNPs. Our results indicate that both types of markers are likely to be useful in population genetics studies and that, in some cases, a combination of SNPs and microsatellites may be the most effective suite of loci.

Keywords: assignment tests, Chinook salmon, differentiation, geetic markers, microsatellites, SNPs

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